What is claimed is:

1. A method of identifying a nucleic acid comprising performing gel or capillary electrophoresis on a series of two or more short sequencing reaction products loaded sequentially onto the same lanes of a sequencing gel, a first sequencing reaction product being loaded at a first loading time and a second short sequencing reaction product being loaded at a second loading time, wherein the first loading time and the second loading time are sufficiently temporally separated to separate the first sequencing reaction product from the second sequencing reaction product by electrophoresis.

2. The method of claim 1, wherein the sequencing reaction product is produced from a region comprising a SNP (single nucleotide polymorphism).

3. The method of claim 1, wherein the sequencing reaction product is produced from an EST (expressed sequence tag).

4. The method of claim 1, wherein the short sequencing reaction products are about 20 bases or shorter.

5. The method of claim 1, wherein the short sequencing reaction products are run off sequencing reaction products.

6. A method of determining the nucleotide sequence of a selected portion of a nucleic acid comprising:

a) isolating the nucleic acid from a nucleic acid library wherein the library comprises a recognition site of a selected enzyme that cuts at least 1 base downstream of the recognition site, wherein the recognition site is positioned within 1 base of the inserts of the library;

b) amplifying the nucleic acid;

c) digesting the amplified nucleic acid with the selected enzyme;

d) performing a run-off sequencing reaction utilizing a primer that hybridizes to a region of the amplified fragment at or upstream of the recognition site to form a first sequencing reaction product; and

e) analyzing the first sequencing reaction product.

7. The method of claim 6, wherein a second sequencing reaction product is analyzed sequentially on the same analysis run as the first sequencing reaction product.

8. The method of claim 6, wherein the selected enzyme is a restriction enzyme.

9. The method of claim 8, wherein the selected restriction enzyme is *BpmI*.

10. The method of claim 6, wherein the analysis performed is gel electrophoresis.

11. The method of claim 6, wherein the analysis is performed with a capillary apparatus.

12. The method of claim 6, wherein the analysis performed is mass spectrophotometry.

13. A kit for performing multiplex analysis of sequencing reactions comprising:

a) an enzyme that cuts at least 1 base downstream of a selected enzyme recognition site; and

b) a set of oligonucleotide linkers comprising a recognition site for the selected enzyme.